

WO 01/09150

PCT/US00/16391

## SEQUENCE LISTING

<110> The Wistar Institute of Anatomy & Biology  
Halazonetis, Thanos  
Scolnick, Daniel

<120> Compositions and Methods to Enhance Sensitivity of  
Cancer Cells to Mitotic Stress

<130> WST97APCT

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<150> 60/146,194

<151> 1999-07-29

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 2679

<212> DNA

<213> Homo sapiens

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<222> (91)..(2082)

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cag tcg ccg ccg ccg cag ccc tgg gga cgg ctc ctg cgt ctg ggc gcg 162
Gln Ser Pro Pro Pro Gln Pro Trp Gly Arg Leu Leu Arg Leu Gly Ala
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gag gag ggc gag ccg cac gtc ctc ctg agg aag cgg gag tgg acc atc 210
Glu Glu Gly Glu Pro His Val Leu Leu Arg Lys Arg Glu Trp Thr Ile
      25              30              35              40

ggg cgg aga cga ggt tgc gac ctt tcc ttc ccc agc aat aaa ctg gtc 258
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Thr Leu Glu Asp Thr Ser Thr Ser Gly Thr Val Ile Asn Lys Leu Lys
      75              80              85

gtt gtt aag aag cag aca tgc cct tta cag act ggg gat gtc atc tac 402
Val Val Lys Lys Gln Thr Cys Pro Leu Gln Thr Gly Asp Val Ile Tyr
      90              95              100

ttg gtg tac agg aag aat gaa ccg gaa cac aac gtg gca tac ctc tat 450
Leu Val Tyr Arg Lys Asn Glu Pro Glu His Asn Val Ala Tyr Leu Tyr
     105              110              115              120

gaa tct tta agt gaa aag caa ggc atg aca caa gaa tcc ttt gaa gct 498
Glu Ser Leu Ser Glu Lys Gln Gly Met Thr Gln Glu Ser Phe Glu Ala
      125              130              135

aac aag gaa aat gtg ttc cat ggg acc aaa gat acc tca ggt gca ggt 546
Asn Lys Glu Asn Val Phe His Gly Thr Lys Asp Thr Ser Gly Ala Gly
      140              145              150

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Ala Gly Arg Gly Ala Asp Pro Arg Val Pro Pro Ser Ser Pro Ala Thr
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cag gtg tgc ttt gag gaa cca cag cca tca aca tcg acg tca gac ctc 642
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ttc ccc aca gcc tcg gcc tct tcc acg gag cct tct cct gca ggg cga 690
Phe Pro Thr Ala Ser Ala Ser Ser Thr Glu Pro Ser Pro Ala Gly Arg
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gag cgt tcc tcc agt tgt ggg tct ggg ggt ggt ggc atc tcc cct aaa 738
Glu Arg Ser Ser Ser Cys Gly Ser Gly Gly Gly Gly Ile Ser Pro Lys
      205              210              215

gga agt ggt ccc tct gtg gca agt gat gaa gtc tcc agc ttt gcc tca 786
Gly Ser Gly Pro Ser Val Ala Ser Asp Glu Val Ser Ser Phe Ala Ser
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gct ctc cca gac aga aag act gcg tcc ttt tcg tcg ttg gaa ccc cag 834
Ala Leu Pro Asp Arg Lys Thr Ala Ser Phe Ser Ser Leu Glu Pro Gln
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Asp Leu Asp Leu Asn Gly Gln Leu Leu Val Ala Gln Pro Arg Arg Asn
265                      270                      275                      280

gcc caa acc gtc cac gag gac gtc aga gca gcg gct ggg aag cca gac      978
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285                      290                      295

aag atg gag gag acg ctg aca tgc atc atc tgc cag gac ctg ctg cac      1026
Lys Met Glu Glu Thr Leu Thr Cys Ile Ile Cys Gln Asp Leu Leu His
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gac tgc gtg agt ttg cag ccc tgc atg cac acg ttc tgc gcg gct tgc      1074
Asp Cys Val Ser Leu Gln Pro Cys Met His Thr Phe Cys Ala Ala Cys
315                      320                      325

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Tyr Ser Gly Trp Met Glu Arg Ser Ser Leu Cys Pro Thr Cys Arg Cys
330                      335                      340

ccc gtg gag cgg atc tgt aaa aac cac atc ctc aac aac ctc gtg gaa      1170
Pro Val Glu Arg Ile Cys Lys Asn His Ile Leu Asn Asn Leu Val Glu
345                      350                      355                      360

gca tac ctc atc cag cat cca gac aag agt cgc agt gaa gaa gat gtg      1218
Ala Tyr Leu Ile Gln His Pro Asp Lys Ser Arg Ser Glu Glu Asp Val
365                      370                      375

caa agt atg gat gcc agg aat aaa atc act caa gac atg ctg cag ccc      1266
Gln Ser Met Asp Ala Arg Asn Lys Ile Thr Gln Asp Met Leu Gln Pro
380                      385                      390

aaa gtc agg cgg cct ttt tct gat gaa gaa ggg agt tca gag gac ctg      1314
Lys Val Arg Arg Ser Phe Ser Asp Glu Glu Gly Ser Ser Glu Asp Leu
395                      400                      405

ctg gag ctg tca gac gtt gac agt gag tcc tca gac att agc cag cca      1362
Leu Glu Leu Ser Asp Val Asp Ser Glu Ser Ser Asp Ile Ser Gln Pro
410                      415                      420

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Leu Gly Asp Ala Pro Ser Thr Ser Val Ser Leu Thr Thr Ala Val Gln
          460                      465                      470

gat tac gtg tgc cct ctg caa gga agc cac gcc ctg tgc acc tgc tgc 1554
Asp Tyr Val Cys Pro Leu Gln Gly Ser His Ala Leu Cys Thr Cys Cys
          475                      480                      485

ttc cag ccc atg ccc gac cgg aga gcg gag cgc gag cag gac ccg cgt 1602
Phe Gln Pro Met Pro Asp Arg Arg Ala Glu Arg Glu Gln Asp Pro Arg
          490                      495                      500

gtc gcc cct cag cag tgt gcg gtc tgc ctg cag cct ttc tgc cac ctg 1650
Val Ala Pro Gln Gln Cys Ala Val Cys Leu Gln Pro Phe Cys His Leu
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tac tgg ggc tgc acc cgg acc ggc tgc tac ggc tgc ctg gcc ccg ttt 1698
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tgt gag ctc aac ctg ggt gac aag tgt ctg gac ggc gtg ctg aac aac 1746
Cys Glu Leu Asn Leu Gly Asp Lys Cys Leu Asp Gly Val Leu Asn Asn
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aac agc tac gag tca gac atc ctg aag aat tac ctg gca acc aga ggt 1794
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ttg aca tgg aaa aac atg ttg acc gag agc ctc gtg gct ctc cag cgg 1842
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gga gtg ttt ctg ctg tct gat tac aga gtc acg gga gac acc gtt ctg 1890
Gly Val Phe Leu Leu Ser Asp Tyr Arg Val Thr Gly Asp Thr Val Leu
          585                      590                      595                      600

tgt tac tgc tgt ggc ctg cgc agc ttc cgt gag ctg acc tat cag tat 1938
Cys Tyr Cys Cys Gly Leu Arg Ser Phe Arg Glu Leu Thr Tyr Gln Tyr
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Arg Gln Asn Ile Pro Ala Ser Glu Leu Pro Val Ala Val Thr Ser Arg
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 635 640 645

cac gcc atg aaa ttc aat cat atc tgt gaa cag aca agg ttc aaa aac 2082  
 His Ala Met Lys Phe Asn His Ile Cys Glu Gln Thr Arg Phe Lys Asn  
 650 655 660

taagcatcca gaggccctga gcagctttca gcactggagg tgaagagagc gtgttttttaa 2142  
 aatacagaga caagcacgtc aaggtgtttt cacagccccc tgagggaagg gacgcagggt 2202  
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 35 40 45  
 Ser Phe Pro Ser Asn Lys Leu Val Ser Gly Asp His Cys Arg Ile Val  
 50 55 60

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Val Asp Glu Lys Ser Gly Gln Val Thr Leu Glu Asp Thr Ser Thr Ser  
65 70 75 80

Gly Thr Val Ile Asn Lys Leu Lys Val Val Lys Lys Gln Thr Cys Pro  
85 90 95

Leu Gln Thr Gly Asp Val Ile Tyr Leu Val Tyr Arg Lys Asn Glu Pro  
100 105 110

Glu His Asn Val Ala Tyr Leu Tyr Glu Ser Leu Ser Glu Lys Gln Gly  
115 120 125

Met Thr Gln Glu Ser Phe Glu Ala Asn Lys Glu Asn Val Phe His Gly  
130 135 140

Thr Lys Asp Thr Ser Gly Ala Gly Ala Gly Arg Gly Ala Asp Pro Arg  
145 150 155 160

Val Pro Pro Ser Ser Pro Ala Thr Gln Val Cys Phe Glu Glu Pro Gln  
165 170 175

Pro Ser Thr Ser Thr Ser Asp Leu Phe Pro Thr Ala Ser Ala Ser Ser  
180 185 190

Thr Glu Pro Ser Pro Ala Gly Arg Glu Arg Ser Ser Ser Cys Gly Ser  
195 200 205

Gly Gly Gly Gly Ile Ser Pro Lys Gly Ser Gly Pro Ser Val Ala Ser  
210 215 220

Asp Glu Val Ser Ser Phe Ala Ser Ala Leu Pro Asp Arg Lys Thr Ala  
225 230 235 240

Ser Phe Ser Ser Leu Glu Pro Gln Asp Gln Glu Asp Leu Glu Pro Val  
245 250 255

Lys Lys Lys Met Arg Gly Asp Gly Asp Leu Asp Leu Asn Gly Gln Leu  
260 265 270

Leu Val Ala Gln Pro Arg Arg Asn Ala Gln Thr Val His Glu Asp Val  
275 280 285

Arg Ala Ala Ala Gly Lys Pro Asp Lys Met Glu Glu Thr Leu Thr Cys  
290 295 300

Ile Ile Cys Gln Asp Leu Leu His Asp Cys Val Ser Leu Gln Pro Cys  
305 310 315 320

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Met His Thr Phe Cys Ala Ala Cys Tyr Ser Gly Trp Met Glu Arg Ser  
325 330 335

Ser Leu Cys Pro Thr Cys Arg Cys Pro Val Glu Arg Ile Cys Lys Asn  
340 345 350

His Ile Leu Asn Asn Leu Val Glu Ala Tyr Leu Ile Gln His Pro Asp  
355 360 365

Lys Ser Arg Ser Glu Glu Asp Val Gln Ser Met Asp Ala Arg Asn Lys  
370 375 380

Ile Thr Gln Asp Met Leu Gln Pro Lys Val Arg Arg Ser Phe Ser Asp  
385 390 395 400

Glu Glu Gly Ser Ser Glu Asp Leu Leu Glu Leu Ser Asp Val Asp Ser  
405 410 415

Glu Ser Ser Asp Ile Ser Gln Pro Tyr Val Val Cys Arg Gln Cys Pro  
420 425 430

Glu Tyr Arg Arg Gln Ala Ala Gln Pro Pro His Cys Pro Ala Pro Glu  
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Gly Glu Pro Gly Ala Pro Gln Ala Leu Gly Asp Ala Pro Ser Thr Ser  
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Val Ser Leu Thr Thr Ala Val Gln Asp Tyr Val Cys Pro Leu Gln Gly  
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Ser His Ala Leu Cys Thr Cys Cys Phe Gln Pro Met Pro Asp Arg Arg  
485 490 495

Ala Glu Arg Glu Gln Asp Pro Arg Val Ala Pro Gln Gln Cys Ala Val  
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Cys Leu Gln Pro Phe Cys His Leu Tyr Trp Gly Cys Thr Arg Thr Gly  
515 520 525

Cys Tyr Gly Cys Leu Ala Pro Phe Cys Glu Leu Asn Leu Gly Asp Lys  
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Cys Leu Asp Gly Val Leu Asn Asn Asn Ser Tyr Glu Ser Asp Ile Leu  
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Lys Asn Tyr Leu Ala Thr Arg Gly Leu Thr Trp Lys Asn Met Leu Thr  
565 570 575

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Glu Ser Leu Val Ala Leu Gln Arg Gly Val Phe Leu Leu Ser Asp Tyr  
 580 585 590

Arg Val Thr Gly Asp Thr Val Leu Cys Tyr Cys Cys Gly Leu Arg Ser  
 595 600 605

Phe Arg Glu Leu Thr Tyr Gln Tyr Arg Gln Asn Ile Pro Ala Ser Glu  
 610 615 620

Leu Pro Val Ala Val Thr Ser Arg Pro Asp Cys Tyr Trp Gly Arg Asn  
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Cys Arg Thr Gln Val Lys Ala His His Ala Met Lys Phe Asn His Ile  
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Lys His Phe Gln Ile Leu Leu Gly Glu Asp Gly Asn Leu Leu Leu Asn  
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Asp Ile Ser Thr Asn Gly Thr Trp Leu Asn Gly Gln Lys Val Glu Arg  
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Asn Ser Asn Gln Leu Leu Ser Gln Gly Asp Glu Ile  
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Tyr Trp Asn Arg Lys Gln Asn Asn Leu Pro Ile Tyr Ile Gly Arg Tyr  
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Thr Glu Arg Tyr Asn Gly Gly Asp Val Ser Ala Ile Val Phe Arg Ser  
20 25 30

Lys Val Val Ser Arg Arg His Ala Gln Ile Phe Tyr Glu Asn Asn Thr  
35 40 45

Trp Tyr Ile Gln Asp Met Gly Ser Ser Ser Gly Thr Phe Leu Asn His  
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Asn Asn Asp Ile Leu  
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35 40 45

Phe Lys Val Asp Ser Gln Gly Asn Trp Tyr Ile Lys Asp Val Lys Ser  
50 55 60

Ser Ser Gly Thr Phe Leu Asn His Gln Arg Leu Ser Pro Ala Ser Ser  
65 70 75 80

Leu Ser Lys Asp Thr Pro Leu Arg Asp Gly Asp Ile Leu  
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35 40

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&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Dmal\_ap

&lt;400&gt; 7

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Val Ala Pro Cys Ser His Ser Tyr His Tyr Lys Cys Ile Arg Pro Thr  
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Leu Asn Glu Ser His Pro Tyr Phe Ser Cys Phe Ile Cys Arg Lys Tyr  
35 40 45

His

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&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; YNL116W\_sc

&lt;400&gt; 8

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Ile Ser Pro Cys Ala His Ser Trp His Phe Arg Cys Val Arg Arg Leu  
20 25 30

Val Met Leu Ser Tyr Pro Gln Phe Val Cys Pro Asn Cys Arg Ser Ser  
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Cys

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&lt;213&gt; Artificial Sequence

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&lt;210&gt; 27

&lt;211&gt; 18

&lt;212&gt; DNA

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&lt;210&gt; 30

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